

METHOD AND SEQUENCES FOR DETERMINATE NUCLEIC ACID HYBRIDIZATION

ABSTRACT OF THE DISCLOSURE

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Provided are methods for using nucleic acid sequences having two or more degenerately pairing nucleotides, each degenerate nucleotide having a partially overlapping set of complementarity, to reduce the number of hybridizing nucleotide sequences or probes used in biochemical and molecular biological operations having sequence specific hybridization. The method may be employed for various hybridization procedures with sequence specific hybridization, including sequencing methods measuring hybridization directly, and tagging by hybridization methods in which the sequence is determined by analyzing the pattern of tags that hybridize thereto, and hybridization dependent amplification methods. The method involves hybridizing to the nucleic acid sequence of interest a first hybridizing nucleotide sequence and a second hybridizing nucleotide sequence, each comprising a sequence complementary, or complementary except at a position of interest or variable position, to a nucleic acid sequence of interest, and analyzing the whether some, all or none of the probes or tags hybridize.

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